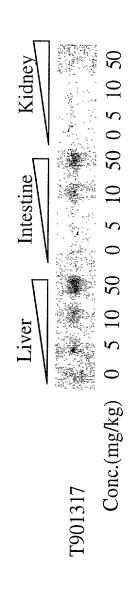
LXR Agonist Compound A Activates the Expression of SSG



Oxysterol and LXR Agonists Activate the Expression of Cholesterol Transporters, ABC1 and ABC8



LXR agonist: C_{pd} B, CFXR agonist: C_{pd} E, F

FIGURE 2

Induction of ABC1 in Liver, Intestine and Kidney of C57BL/6 Mice by LXRa Agonist God A

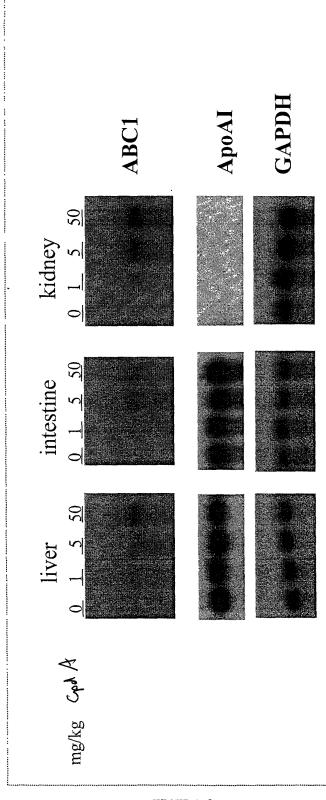
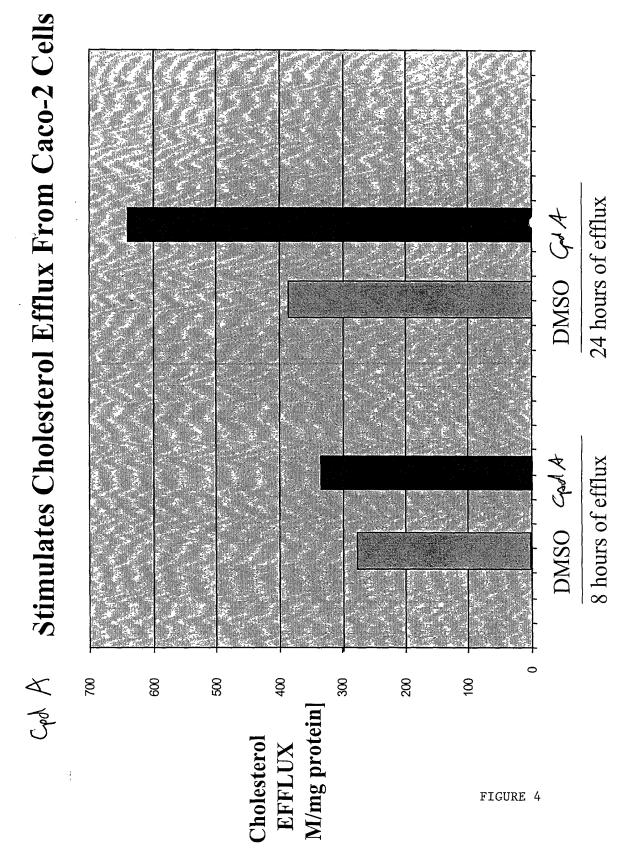
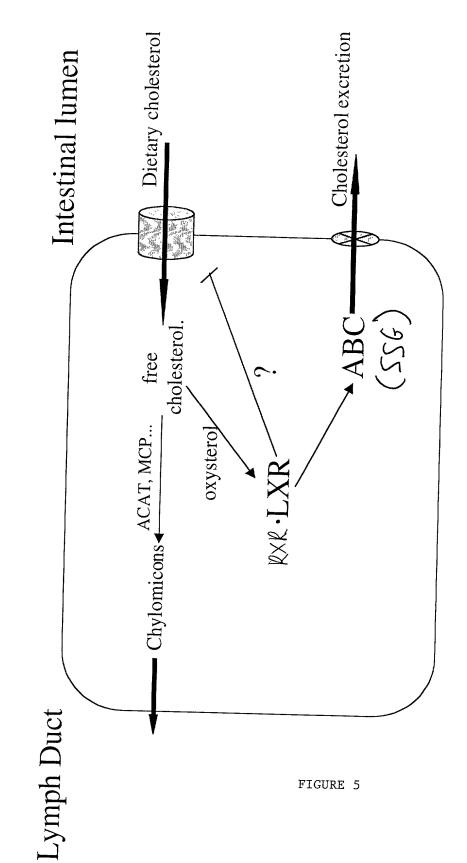


FIGURE 3



How Does LXR Regulate Cholesterol Absorption? -A Working Model -



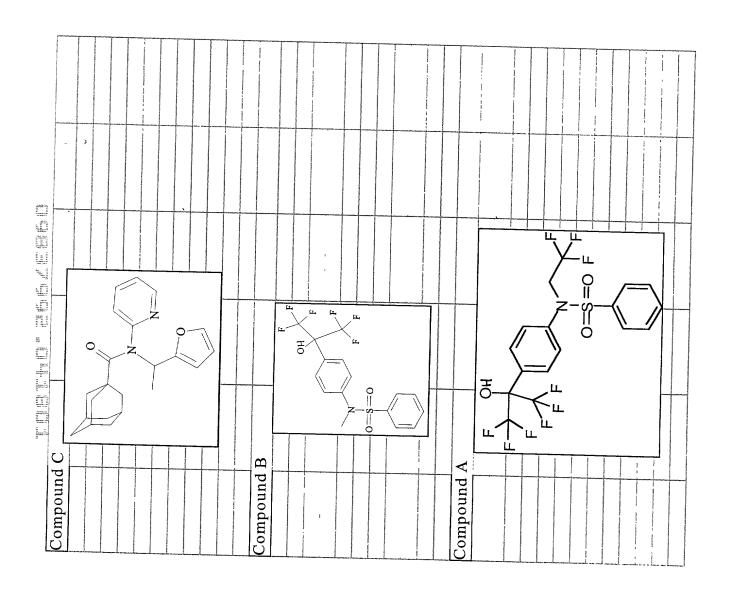


FIGURE 6

225 TCGGCACAGCTTAGGRCTCCTACATGTGTCCACACCGTGTCGGGACCTTGGTGGAACATCAAATCATGCCAGCAGAAGTGGGGACAGGCAAATCCTCAAAGATGTCCTTGTACATGCGAGAGTGGCCCAGATTATGTGCAT R H S L G V L H V S Y S V S N R V G P W W N I K S C Q Q K W D R Q I L K D V S L Y I E S G Q I M C I>

525 GAGCGACGITTITCTGAGCACCTCACTGCGCAGACATACCAGCGATGCTGGCCCTCTGCCGCAGCTTCTACAACAAGAAGTAGAGGCAGTCATGACAGAGCTGAGCCTGAGCCAGTGGCGGCGAAAA S D V F L S S L T V R E T L R Y T A M L A L C R S S A D F Y N K K V E A V M T E L S L S H V A D Q W

CATGETCAATGETGAATCTGTTTCCCATGAGACCOTCAGGAGACTCAGGAGACTCAGTATCATAAGTGGCAGATGCTGCTCGCCTACAGGGTCTTCAGCGTCATCGCCACGGTCATTTTCAGCAA Σ

TO C Y W T L G L Y P E V A R F G Y F S A A L L A P H L I G E F L T L V L L G I V Q N P N I V N S I V

CHICACTIGIGARICCAACACCICIALGCIAAAICACCGAAGATGCGGCAACAGAGGGGCCCAAGAGAAAAACCTGCCAGGATCACGGGCAAACTICCTCAACTTATATGGGTTTATCCCAGCTCT F 1 C G G S N T S M L N H P M C A I T Q G V Q F I E K T C P G A T S R F T A N F L I L Y G F I P A L

2550 CCITGEOCITGEOCITICIGE COARGO COA A GAGA CA GAGA CA CA CA CA CA CA CA CA CA CATA CA CATA CA CATA CA CATA CATA A TA A

FIGURE 7

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د
                                                                                                                       CCAAGTAAACAGAGGTCCCTGGAGGGGGCTCCTGCCACCCCGGAGGCTCACAGCCTGGGCATCCTCCAAGGGTCAGCGGTCAGGCGTGAGGCCCTGGTGGAAAATCACATCTTGCCGGCAGCAGTGGAC
Q V N R G S Q S S L E G A P A T A P E P H S L G I L H A S Y S V S H R V R P W W D I T S C R Q Q W T>
GICAGGIGGAGCAGGCAGGGCACCGGGCCACCGAGCCACTCTGGGGAGGGTCGGGCACCACCAGAAAITIGCCCAGCTITGCTGCTTGGCCATGGTGACCTCTCATCTTGACCCCCGGAGGGTCCATGGGTCT
N G D L S S L T P G G S M G L>
                                                                                                                                                                                                                             825
F D E P T T G L D C M T A N Q I V V L L V E L A R R N R I V V L T I H Q P R S E L F Q L F D K I A I>
                                                                                                                                                                                                                                                                                                                                                                                                            GAAGAAGGTGGAAGGCGATGAGGCGATGTGGGACTGATTGGCACTGATTGGCAGGGATTTCCAGGGGTAAGCGGGGGCGTGAGGGGGGTCTCCATGGAGGCGAGCCAGGTGTGGAAGGTCATAGGTCATGGT
K k v e a v m a e l s l s h v a d r l i g n y s l g g i s t g e r r v s i a a q l l q d p r v m l>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATAGAAACCTCCAAGAGAGTCCAGAATGCTGCCTACAAGAAATCAGCAATTIGTCATAAAAGAATATTGAAAGAATGAATGAAGAATGATAACAAAAAGTTACCAATGGTTCCTTTCAAAACCAAAAGTTTTTT E S K R V Q M I E S A Y K K S A I C H K T L K N I E R M K H L K T L P M V P F K T K D S P G V F>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATCCAGGACGGCGTAGGTCCTTTACCAGTTYGTGGGGGCCACCCGTACACAGGCTGTGAATCTGTTTCCCGTGCTGCTGGCGAGTGTGGGAGTCAGGAGTCAGGACGTCTACCAGAAGTGGCAGATGATGCT
I Q D R V G L L Y Q F V G A T P Y T G M L N A V N L F P V L R A V S D Q E S Q D G L Y Q K W Q M M L>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTAACTCTTGTGCTACTAGGAATATCAAATATAGTCAACAGTGTAGGGCTCTGCCATTGCCGGGGGGTTCTTGCAATTCCTCAGAAACATACAAAATGCCCATTCCTTTTAAAATCATCAGTAATTT
L T L V L L G I V Q N P N I V N S V V A L L S I A G V L V G S G F L R N I Q E M P I P F K I I S Y F>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACATICCAAAAATHATAGAGAGATICTIGTAGAGACTGAATICTAGAGACTCAAATGTTTCTGTGACAACTAATCCAATGTGTGGCTTCACTCAAGGAATTCAATGAGAAAACTGCCCAGG
T F Q K Y C S E I L V V N E F Y G L N F T C G S S N V S V T T N P M C A F T Q G I Q F I E K T C P G:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCAACATCTAGATTCACAATGAACTTTCTGATTTTATTCCAGCTCTTGTCATCCTAGGAATTGTTTTCAAAATAAGGGAATCATCTCATTAGCAGGTAGTGAAAGCCATGGCTAGGGAAAATGGAAGCTGCCA
A T S R F T M N F L I L Y S F I P A L V I L G I V V F K I R D H L I S R X>
```

FIGURE 8

ttgcticttacaacittgcaggacatgtggttatttggaaattgtgactgagggaaccgaagaatgtaaatrataattataaacctatggg

Alignment of Human and Mouse SSG Protein Sequences

hSSG.pro	MGDLSSLTPG GSMGLQVNRG SQSSLEGAPA TAPEP-HSLG ILHASYSVSH	49
mSSG.pro	MGELPFLSPE GARGPHINRG SLSSLEQGSV TGTEARHSLG VLHVSYSVSN	50
hSSG.pro	RVRPWWDITS CRQQWTRQIL KDVSLYVESG QIMCILGSSG SGKTTLLDAM	99
mSSG.pro	RVGPWWNIKS CQQKWDRQIL KDVSLYIESG QIMCILGSSG SGKTTLLDAI	100
hSSG.pro	SGRLGRAGTF LGEVYVNGRA LRREQFODCF SYVLQSDTLL SSLTVRETLH	149
mSSG.pro	SGRLRRTGTL EGEVFVNGCE LRRDQFODCF SYVLQSDVFL SSLTVRETLR	150
hSSG.pro	YTALLAIRRG NPGSFQKKVE AVMAELSLSH VADRLIGNYS LGGISTGERR	199
mSSG.pro	YTAMLALCRS SADFYNKKVE AVMTELSLSH VADQMIGSYN FGGISSGERR	200
hSSG.pro	ŔVŚĮAĄQĿĿQ DPĸVMLFDEP ŢŢĠĿDCMŢĄN QĮVVLLVĖLA RŖNRĖVVLTI	249
mSSG.pro	ŖVSĮĄĄQĿĿQ DPĸVMLDEP ŢŢŖĿDCMŢĄN QĮVLĿĻAĘĿĄ ŖŖDŔĮVIVŢI	250
hSSG.pro	HOPRSELFOL FOKIATLSFG ELIFCGTPAE MLDFFNDCGY PCPEHSNPFD	299
mSSG.pro	HOPRSELFOH EDKIATLITYG ELVECGTPEE MLGFFNNCGY PCPEHSNPFD	300
hSSG.pro mSSG.pro	FYMDLÍTSVOT OSREREIFTY KRÝOMLECAF KESDIYHKIL ENTERARYLK	349 350
hSSG.pro	TIPMVPFKTK DSPGVFSKLG VILRRVTRNI VRNKLAVITR LLONLIMGLF	399
mSSG.pro	TLPMVPFKTK DPPGMFGKLG VILLRRVTRNI MRNKQAVIMR IVONLIMGLF	400
hSSG.pro	LLEFVLRVRS NVĽKGAIQDR VGLLYQFVGA TPYTGMLNAV NLFPVLRAVS	449
mSSG.pro	LIFYLLRVQN NTĽKGAVQDR VGELYQLVGA TPYTGMLNAV NLFPMLRAVS	450
hSSG.pro	DOESODGLYO KWOMLAYAL HVLPFSVVAT MIFSSVCYWT LGLHPEVARF	499
mSSG.pro	DOESODGLYH KWOMLLAYVI HVLPFSVIAT VIFSSVCYWT LGLYPEVARF	500
hSSG.pro	ĠŶĘŚĄĄĹĹĄP HLIGEFLTLV LLĠIVONPNI VNŚVVALLŚI AGVLVGŚGFL	549
mSSG.pro	ĠŶŖŚĄĄĹĿĄP HUIGEFTTLV LUGIVONPNI VNŚIVAŁLŚI SGLEIGSGFI	550
hSSG.pro	RNIOEMPIPF KIISYFTFOK YCCEILVVNE FYGLNFTCGS SNVSVTTNPM	599
mSSG.pro	RNIOEMPIPL KILGYFTFOK YCCEILVVNE FYGLNFTCGG SNTSMLNHPM	600
hSSG.pro	CAFTOGLOFI EKTCPGATSR FTMNFLILYS FIPALVILGE VIFKVRDYLI	649
mSSG.pro	CALTOGVOFI EKTCPGATSR FTANFLILYG FIPALVILGE VIFKVRDYLI	650
hSSG.pro	SR	651
mSSG.pro	SR	652

Reference Number: 6711 Stanford RH Panel: TNG4 Lowest LOD Reported: 6 Chromosome Value: 0

Results for HT

Submitted

SHGCNAME CHROM# LOD_SCORE DIST.(cRs)

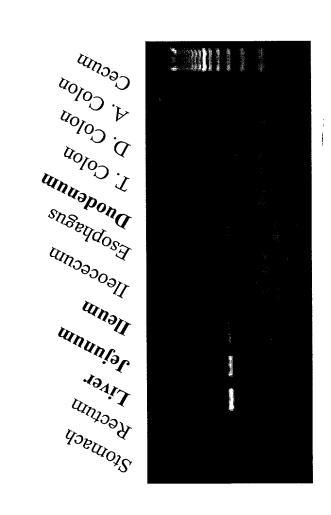
1 SHGC-36672 2 7.52 35

2 SHGC-8189 2 6.53 44

3 SHGC-699 2 6.03 48

The number of markers searched was 32440.

in the GI Tract Expression Profile of St



Small Intestine

Stomach

Jejunum

Jejunum

Lecum

Reccum

Colon

EICHE II

is Predominantly Expressed the Liver and Small Intestine 25 Human

Spleen Testis Thymus S. Intestine Prostate 78_d N_ENO CO/01 S. Muscle eju_{eob}ld b^{gUCL6g8} SUNT FINGL Brain Kidney Kidney

FIGURE 12

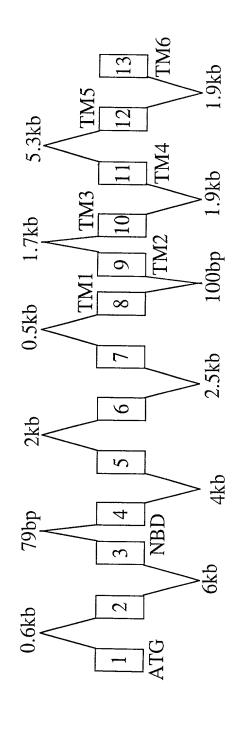
is Selectively Expressed in the Liver and Small Intestine 256 Mouse

S. Intestine S. Intestine Spleen Lung Spleen Lung Spleen Liver Brain sunvit S. Muscle Sitset Skin

Mouse Multiple Tissue RT-PCR

cDNA Cloning and Genomic Organization of $\S\S\S$

- The predicted human and mouse proteins share 80% identity and is 28% identical to Drosophila Brown
- Human ABCG5 contains 13 exons and spans at least 25kb of genomic DNA



Human SSG nucleotide sequence—13 Exons

Exon 1 GTCAGGTGGAGCAGGCAGGCAGTCTGCCACGGGCTCCCCAACTGAAGCCACTCTGGGGA GGGTCCGGCCACCAGAAAATTTGCCCAGCTTTGCTGCCTGTTGGCCATGGGTGACCTCTC ATCTTTGACCCCGGAGGGTCCATGGGTCTCCAAGTAAACAGAGGCTCCCAGAGCTCCCT CAGGCAGATCCTCAAAGATGTCTCCTTGTACGTGGAGAGCGGGCAGATCATGTGCATCCT AGGAAGCTCAGGCTCCGGGAAAACCACGCTGCTGGACGCCATGTCCGGGAGGCTGGGGCG CGCGGGGACCTTCCTGGGGGAGGTGTATGTGAACGGCCGGGCGCTGCGCCCGGGAGCAGTT CCCTGCTGAGCAGCCTCACCGTGCG GAAGAAGGTGCAGCCGTCATGGCAGAGCTGAGTCTGAGCCATGTGGCAGACCGACTGAT CCACGGGTGAGCGGCGCCGGGTCTCCATCGCAGC TAAGGTCATGCTGTTTGATGAGCCAACCACAGGCCTGGACTG CCTGAGCTTCGGAGAGCTGATTTTCTGTGGCACGCCAGCGGAAATGCTTGA TGACTGCGGTTACCCTTGTCCTGAACATTCAAACCCTTTTGACTTCTATATGĞÂCCTGAC GTCAGTGGATACCCAAAGCAAGGAACGGGAAATAGAAACCTCCAAGAGAGTCCAGATGAT AGAATCTGCCTACAAGAAATCAGCAATTTGTCATAAAACTTTGAAGAATATTGAAAGAAT GAAACACCTGAAAACGTTACCAATGGTTCCTTTCAAAACCAAAGATTCTCCTGGAGTTTT \mathbf{r} \mathbf{ENON} \mathbf{q} CTCTAAACTGGGTGTTCTCCTGAGGAGGTGACAAGAAACTTGGTGAGAAATAAGCTGGC AGTGATTACGCGTCTCCTTCAGAATCTGATCATGGGTTTGTTCCTCCTTTTTCTTCGTTCT GCGGGTCCGAAGCAATGTGCTAAAGGGTGCTATCCAGGACCGC GTTTGTGGGCGCCACCCCGTACACAGGCATGCTGAACGCTGTGAATCTG GCGAGCTGTCAGCGACCAGGAGAGTCAGGACGGCCTCTACCAGAAGTGGCAGATGATGCT GCAÇTGCACGTCCTCCCCTTCAGCGTTGTTGCCACCATGATTTTCAGCAGTGT CTTACATCCTGAGGTTGCCCGATTTGGATATTTTTCTGCTGC TCTCTTGGCCCCCCACTTAATTGGTGAATTTCTAACTCTTGTGCTACTTGGTATCGTCCA AAATCCAAATATAGTCAACAGTGTAGTGGCTCTGCTGTCCATTGCGGGGGTGCTTGTTGGATCTGGATTCCTCAGAAAATGCCCATTCCTTTTAAAATCATCAGTTATTT TACATTCCAAAAATATTGCAGTGAGATTCTTGTAGTCAATGAGTTCTACGGACTGAATTT ÄĞCTCAAATGTTTCTGTGACAACTAATCCAATGTGTGCCTTCACTCAAGG AATTCAATTCATTGAGAAAACCTGCCCAGGTGCAACATCTAGATTCACAATGAACTTTCT

	Exon number	exon size	5' splicing site	3' splicing site	Intron size		
	1 ·			GCGTCAGgtaaggcag	~600bp		
	2	124	cctttaaagCCACCGC	AGCTCAGgtaagcttg	~6kb		
	3	137	gccccgcagGCTCCGG	CCTGCAGgtgggcgcg	79bp		
	4	103	ctcctgcagAGCGACA	AAGGTGGgtgcagccc	~4kb		
	5	129	tgcaggtggAGGCCGT	GATCCTAgtaagtggc	~2kb		
	6	140	tgctggcagAGGTCAT	TTTTCAGgtaagaggt	~2.5kb		
	7	130	tctggtcagCTCTTTG	TTCTATAgtaagtttt	~0.5kb		
	8	214	aacttttagTGGACCT	TCCTGAGgtaagaggc	100bp		
	9	206	tgttttcagGAGAGTG	AATCTGTgtaagtgcc	~1.7kb		
	10	139	catccccagTTCCCGT	GCTACTGgtgaggggtt	~1.9kb		
	11	186	cttttctagGACGCTG	TCCTCAGgtaagatat	~5.3kb		
	12	113	tttcttaagAAACATA	ACTTGTGgtaagtatt	~1.2kb		
	13		ccttgacagGCAGCTC	5 5 ··· ··			
	Total				~25.9kb		
Exonic sequences in capital latter							

Exonic sequences in capital letter

FIGURE 14B (2 of 2)